

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/045781
Source: 1FW
Date Processed by STIC: 12/3/4

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 12/03/2004

PATENT APPLICATION: US/10/645,784

TIME: 12:08:58

Input Set : N:\Crif3\RULE60\10645784.raw

Output Set: N:\CRF4\12032004\J645784.raw

```

1 <110> APPLICANT: FEIGE, ULRICH
2   LIU, CHUAN-FA
3   CHEETHAM, JANET C.
4   BOONE, THOMAS CHARLES
5   GUDAS, JEAN MARIE
6 <120> TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
7 <130> FILE REFERENCE: A-527A
8 <140> CURRENT APPLICATION NUMBER: US/10/645,784
9 <141> CURRENT FILING DATE: 2003-08-18
10 <150> PRIOR APPLICATION NUMBER: US/09/563,286
11 <151> PRIOR FILING DATE: 2000-05-03
12 <150> PRIOR APPLICATION NUMBER: 09/428,082
13 <151> PRIOR FILING DATE: 1999-10-22
14 <150> PRIOR APPLICATION NUMBER: 60/105,371
15 <151> PRIOR FILING DATE: 1998-10-23
16 <160> NUMBER OF SEQ ID NOS: 1157
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 684
21 <212> TYPE: DNA
22 <213> ORGANISM: HUMAN
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1)..(684)
26 <223> OTHER INFORMATION:
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29   Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
30   1          5          10          15
31   ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc      96
32   Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
33   20          25          30
34   atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc      144
35   Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
36   35          40          45
37   cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag      192
38   His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
39   50          55          60
40   gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg      240
41   Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
42   65          70          75          80
43   tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat      288
44   Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn

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45          85          90          95
46 ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc 336
47 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
48          100          105          110
49 atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag 384
50 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
51          115          120          125
52 gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc 432
53 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
54          130          135          140
55 agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg 480
56 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
57          145          150          155          160
58 gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct 528
59 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
60          165          170          175
61 ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc 576
62 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
63          180          185          190
64 gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg 624
65 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
66          195          200          205
67 atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg 672
68 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
69          210          215          220
70 tct ccg ggt aaa 684
71 Ser Pro Gly Lys
72 225
74 <210> SEQ ID NO: 2
75 <211> LENGTH: 228
76 <212> TYPE: PRT
77 <213> ORGANISM: HUMAN
78 <400> SEQUENCE: 2
79 Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
80 1 5 10 15
81 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
82 20 25 30
83 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
84 35 40 45
85 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
86 50 55 60
87 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
88 65 70 75 80
89 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
90 85 90 95
91 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
92 100 105 110
93 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
94 115 120 125

```

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```

95      Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
96      130                      135                      140
97      Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
98      145                      150                      155                      160
99      Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
100     165                      170                      175
101     Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
102     180                      185                      190
103     Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
104     195                      200                      205
105     Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
106     210                      215                      220
107     Ser Pro Gly Lys
108     225

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110 <210> SEQ ID NO: 3

111 <211> LENGTH: 36

112 <212> TYPE: PRT

113 <213> ORGANISM: Artificial Sequence

114 <220> FEATURE:

115 <223> OTHER INFORMATION: PEPTIDE SEQUENCE MODIFIED FOR PEGYLATION

116 <220> FEATURE:

117 <221> NAME/KEY: misc_feature

118 <222> LOCATION: (18)..(18)

119 <223> OTHER INFORMATION: Methoxy-polyethylene glycol (5000 Dalton)-sulfoacetyl group
 attac

120 hed to the sidechain.

121 <400> SEQUENCE: 3

122 Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly

123 1 5 10 15

124 Gly Lys Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu

125 20 25 30

126 Ala Ala Arg Ala

127 35

129 <210> SEQ ID NO: 4

130 <211> LENGTH: 36

131 <212> TYPE: PRT

132 <213> ORGANISM: Artificial Sequence

133 <220> FEATURE:

134 <223> OTHER INFORMATION: PEPTIDE SEQUENCE MODIFIED FOR PEGYLATION

135 <220> FEATURE:

136 <221> NAME/KEY: misc_feature

137 <222> LOCATION: (18)..(18)

138 <223> OTHER INFORMATION: Methoxy-polyethylene glycol (5000 Dalton)-succinimidyl group
 att

139 ched to the sidechain.

140 <400> SEQUENCE: 4

141 Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala Gly Gly

142 1 5 10 15

143 Gly Cys Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu

144 20 25 30

145 Ala Ala Arg Ala

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Input Set : N:\Crf3\RULE60\10645784.raw

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146          35
148 <210> SEQ ID NO: 5
149 <211> LENGTH: 794
150 <212> TYPE: DNA
151 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
153 <223> OTHER INFORMATION: Fc-TMP
154 <220> FEATURE:
155 <221> NAME/KEY: CDS
156 <222> LOCATION: (39)..(779)
157 <223> OTHER INFORMATION:
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159      tctagatttg ttttaactaa ttaaaggagg aataacat atg gac aaa act cac aca      56
160                                     Met Asp Lys Thr His Thr
161                                     1          5
162      tgt cca cct tgt cca gct ccg gaa ctc ctg ggg gga ccg tca gtc ttc      104
163      Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
164                                     10          15          20
165      ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct      152
166      Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
167                                     25          30          35
168      gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc      200
169      Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
170      40          45          50
171      aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca      248
172      Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
173      55          60          65          70
174      aag ccg cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc      296
175      Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
176      75          80          85
177      ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc      344
178      Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
179      90          95          100
180      aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc      392
181      Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
182      105          110          115
183      aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca      440
184      Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
185      120          125          130
186      tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc      488
187      Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
188      135          140          145          150
189      aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg      536
190      Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
191      155          160          165
192      cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac      584
193      Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
194      170          175          180
195      ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg      632

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196   Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
197           185                      190                      195
198   cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac      680
199   Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
200           200                      205                      210
201   aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa ggt gga      728
202   Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly
203           215                      220                      225                      230
204   ggt ggt ggt atc gaa ggt ccg act ctg cgt cag tgg ctg gct gct cgt      776
205   Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg
206           235                      240                      245
207   gct taatctcgag gatcc      794
208   Ala
210 <210> SEQ ID NO: 6
211 <211> LENGTH: 247
212 <212> TYPE: PRT
213 <213> ORGANISM: Artificial Sequence
214 <220> FEATURE:
215 <223> OTHER INFORMATION: Fc-TMP
216 <400> SEQUENCE: 6
217   Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
218   1           5                      10                      15
219   Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
220           20                      25                      30
221   Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
222           35                      40                      45
223   His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
224           50                      55                      60
225   Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
226           65                      70                      75                      80
227   Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
228           85                      90                      95
229   Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
230           100                     105                     110
231   Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
232           115                     120                     125
233   Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
234           130                     135                     140
235   Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
236           145                     150                     155                     160
237   Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
238           165                     170                     175
239   Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
240           180                     185                     190
241   Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
242           195                     200                     205
243   Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
244           210                     215                     220
245   Ser Pro Gly Lys Gly Gly Gly Gly Gly Gly Ile Glu Gly Pro Thr Leu Arg

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/645,784

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Input Set : N:\Crf3\RULE60\10645784.raw
Output Set: N:\CRF4\12032004\J645784.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:33; Xaa Pos. 6,7,8
Seq#:45; Xaa Pos. 8,9,10
Seq#:56; Xaa Pos. 8,9
Seq#:57; Xaa Pos. 8,9,10
Seq#:58; Xaa Pos. 8,9,10,11
Seq#:59; Xaa Pos. 8,9,10,11,12
Seq#:60; Xaa Pos. 8,9,10,11,12,13
Seq#:71; Xaa Pos. 2,12
Seq#:72; Xaa Pos. 2,3,13
Seq#:73; Xaa Pos. 2,12,13
Seq#:74; Xaa Pos. 2,3,13,14
Seq#:83; Xaa Pos. 2,4,5,8,11,13
Seq#:84; Xaa Pos. 2,4,5,8,11,13,16,18,19,22,25,27
Seq#:85; Xaa Pos. 2,4,5,8,11,13
Seq#:86; Xaa Pos. 2,4,5,8,11,13
Seq#:100; Xaa Pos. 4
Seq#:101; Xaa Pos. 1,5
Seq#:102; Xaa Pos. 1,4
Seq#:104; Xaa Pos. 4
Seq#:124; Xaa Pos. 1,2,3,6,9,10
Seq#:142; Xaa Pos. 2,4,8,9
Seq#:212; Xaa Pos. 1,2,3,5,7,8,9
Seq#:221; Xaa Pos. 10
Seq#:222; Xaa Pos. 10
Seq#:223; Xaa Pos. 11
Seq#:224; Xaa Pos. 10
Seq#:225; Xaa Pos. 10
Seq#:226; Xaa Pos. 10
Seq#:227; Xaa Pos. 10
Seq#:228; Xaa Pos. 10
Seq#:229; Xaa Pos. 6,10
Seq#:230; Xaa Pos. 6,10
Seq#:234; Xaa Pos. 5,10
Seq#:235; Xaa Pos. 5,10
Seq#:236; Xaa Pos. 6,10
Seq#:237; Xaa Pos. 5,10
Seq#:240; Xaa Pos. 10
Seq#:241; Xaa Pos. 10
Seq#:242; Xaa Pos. 8,10
Seq#:243; Xaa Pos. 10
Seq#:244; Xaa Pos. 10
Seq#:245; Xaa Pos. 10
Seq#:246; Xaa Pos. 10
Seq#:247; Xaa Pos. 10

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : N:\Crf3\RULE60\10645784.raw
Output Set: N:\CRF4\12032004\J645784.raw

Seq#:248; Xaa Pos. 10
Seq#:249; Xaa Pos. 6,10
Seq#:253; Xaa Pos. 10
Seq#:254; Xaa Pos. 5,10
Seq#:255; Xaa Pos. 6,10
Seq#:256; Xaa Pos. 5,10
Seq#:258; Xaa Pos. 1,10

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:3; Line(s) 119
Seq#:4; Line(s) 138
Seq#:26; Line(s) 1083,1087
Seq#:27; Line(s) 1101
Seq#:28; Line(s) 1115,1120
Seq#:29; Line(s) 1137
Seq#:30; Line(s) 1155
Seq#:31; Line(s) 1170
Seq#:32; Line(s) 1189,1193
Seq#:85; Line(s) 1789
Seq#:93; Line(s) 1895
Seq#:96; Line(s) 1937
Seq#:97; Line(s) 1953
Seq#:98; Line(s) 1971
Seq#:99; Line(s) 1986
Seq#:100; Line(s) 2001
Seq#:103; Line(s) 2048
Seq#:104; Line(s) 2062
Seq#:124; Line(s) 2270,2282,2291
Seq#:275; Line(s) 4171
Seq#:320; Line(s) 4721
Seq#:377; Line(s) 5471
Seq#:378; Line(s) 5480
Seq#:379; Line(s) 5489
Seq#:380; Line(s) 5498
Seq#:381; Line(s) 5507
Seq#:382; Line(s) 5516
Seq#:383; Line(s) 5525
Seq#:386; Line(s) 5574
Seq#:387; Line(s) 5585
Seq#:388; Line(s) 5594
Seq#:389; Line(s) 5617
Seq#:398; Line(s) 5737
Seq#:419; Line(s) 5973
Seq#:421; Line(s) 6026
Seq#:448; Line(s) 6349
Seq#:461; Line(s) 6516

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Input Set : N:\Crf3\RULE60\10645784.raw
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Seq#:473; Line(s) 6674
Seq#:592; Line(s) 8022,8026,8031
Seq#:593; Line(s) 8048
Seq#:594; Line(s) 8065,8070,8074
Seq#:909; Line(s) 11479,11483
Seq#:910; Line(s) 11517,11521
Seq#:917; Line(s) 11671
Seq#:1042; Line(s) 13457,13467,13487
Seq#:1110; Line(s) 14871
Seq#:1142; Line(s) 15203,15207,15212,15216
Seq#:1143; Line(s) 15232,15236,15241,15245
Seq#:1144; Line(s) 15261,15265,15270,15274
Seq#:1145; Line(s) 15290,15294,15299,15303
Seq#:1146; Line(s) 15319,15323,15328,15332

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10645784.raw

Output Set: N:\CRF4\12032004\J645784.raw

L:27 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:0
L:158 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:0
L:260 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:0
L:368 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:0
L:476 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:0
L:602 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:0
L:705 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:0
L:808 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:19,Line#:0
L:919 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:0
L:1210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
L:1334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0
L:1448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:0
L:1462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:0
L:1476 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0
L:1490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59 after pos.:0
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L:1632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72 after pos.:0
L:1646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73 after pos.:0
L:1660 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74 after pos.:0
L:1761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:0
L:1775 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84 after pos.:0
M:341 Repeated in SeqNo=84
L:1795 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:0
L:1809 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:0
L:2004 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:100 after pos.:0
L:2020 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101 after pos.:0
L:2036 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:102 after pos.:0
L:2068 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:104 after pos.:0
L:2294 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:124 after pos.:0
L:2480 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:142 after pos.:0
L:3255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:212 after pos.:0
L:3360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:221 after pos.:0
L:3375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:222 after pos.:0
L:3389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:223 after pos.:0
L:3403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:224 after pos.:0
L:3417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:225 after pos.:0
L:3431 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:226 after pos.:0
L:3445 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:227 after pos.:0
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L:3580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:237 after pos.:0
L:3624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:240 after pos.:0
L:3646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:241 after pos.:0

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Output Set: N:\CRF4\12032004\J645784.raw

L:3668 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:242 after pos.:0
L:3686 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:243 after pos.:0
L:3704 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:244 after pos.:0
L:3722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:245 after pos.:0
L:3740 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:246 after pos.:0
L:3762 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:247 after pos.:0
L:3784 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:248 after pos.:0
L:3806 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:249 after pos.:0
L:3867 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:253 after pos.:0
L:3891 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:254 after pos.:0
L:3909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:255 after pos.:0
L:5347 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:367,Line#:0
L:5441 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:375,Line#:0
L:5539 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:384,Line#:0
L:5688 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:394,Line#:0
L:5781 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:402,Line#:0
L:5924 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:416,Line#:0
L:13663 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1055,Line#:0
L:13763 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1057,Line#:0
L:13863 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1059,Line#:0
L:13963 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1061,Line#:0
L:14063 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1063,Line#:0
L:14164 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1065,Line#:0
L:14265 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1067,Line#:0
L:14364 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1069,Line#:0
L:14983 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1120,Line#:0